

Dense subgraph mining with a mixed graph model

Anita Keszler*

*Distributed Events Analysis Laboratory, Computer and Automation Research Institute
(MTA SZTAKI), H-1111, Kende u. 13-17, Budapest, Hungary*

Tamás Szirányi

Distributed Events Analysis Laboratory, MTA SZTAKI

Zsolt Tuza

*Alfréd Rényi Institute of Mathematics, Hungarian Academy of Sciences
Department of Computer Science and Systems Technology, University of Pannonia*

Abstract

In this paper we introduce a graph clustering method based on dense bipartite subgraph mining. The method applies a mixed graph model (both standard and bipartite) in a three-phase algorithm. First a seed mining method is applied to find seeds of clusters, the second phase consists of refining the seeds, and in the third phase vertices outside the seeds are clustered. The method is able to detect overlapping clusters, can handle outliers and applicable without restrictions on the degrees of vertices or the size of the clusters. The running time of the method is polynomial. A theoretical result is introduced on density bounds of bipartite subgraphs with size and local density conditions. Test results on artificial datasets and social interaction graphs are also presented.

Keywords: graph clustering, mixed graph model, dense subgraph mining, cluster seed mining, social graphs

*Corresponding author. Tel.: +36 12796106.

Email addresses: keszler.anita@sztaki.mta.hu (Anita Keszler),
sziranyi.tamas@sztaki.mta.hu (Tamás Szirányi), tuza.zsolt@renyi.mta.hu (Zsolt Tuza)
Preprint submitted to Pattern Recognition Letters April 2, 2013

13 1. Introduction

14 Data clustering is one of the most rapidly developing area of machine learn-
15 ing. Among the several main stream techniques (see Jain (2010) for a detailed
16 introduction), graph based clustering methods have gained a lot of attention
17 since the previous decades in numerous engineering applications (see for exam-
18 ple Geva and Sharan (2011), Benchettara et al. (2010), Boykov and Kolmogorov
19 (2004), Cousty et al. (2009), Du et al. (2008)), due to the modeling capabili-
20 ties of graphs, and the large number of available theoretical results in this field
21 (Schaeffer (2007)).

22 Considering the modeling, there are two major types of graph based clus-
23 tering methods used in the field of pattern recognition: standard and bipartite
24 graphs. Standard graphs model the objects to be clustered, bipartite graphs
25 - with the two vertex classes - are eligible to model properties of the objects
26 as well (Geva and Sharan (2011)). Some applications apply projection of the
27 bipartite graph to standard graphs (e.g. Benchettara et al. (2010)).

28 Frequently applied methods using the standard model are graph partition-
29 ing and dense subgraph mining methods. Graph cuts (Boykov and Kolmogorov
30 (2004), Danek et al. (2012), Cousty et al. (2010)), spectral partitioning, several
31 MST-based clustering methods such as Zhou et al. (2011) belong to the parti-
32 tioning methods. On the other hand, clique mining (Feige (2004)) is an example
33 of density based methods.

34 In case of bipartite graph models, there also exist partitioning methods which
35 divide one or both vertex classes into disjoint subsets (e.g. modularity-based

36 methods, such as Barber et al. (2008)), however dense subgraph mining methods
37 - e.g. biclustering, dense bipartite subgraph mining (Du et al. (2008), Jancura
38 and Marchiori (2010)) - are applied more often.

39 The advantage of the partitioning methods is their low computational cost
40 (polynomial in the number of vertices). One of their drawbacks is that these
41 algorithms are not able to deal with overlaps between clusters. Outliers cannot
42 be handled either, therefore, pairwise similarities within a cluster cannot be
43 ensured.

44 Density based methods are designed to overcome these drawbacks, but with
45 exponential running time in the number of vertices - in general. In case of
46 restrictions of vertex degrees, or limitations on the expected cluster sizes, there
47 exist more efficient algorithms.

48 These methods are applied even if all the vertices are needed to be clustered.
49 Dense subgraphs are considered as seeds of clusters, and the remaining vertices
50 are clustered based on their similarities to the cluster seeds Du et al. (2008),
51 Jancura and Marchiori (2010).

52 However, for bipartite graphs it is also proven that for a wide range of edge
53 weights even finding good approximations of the maximum weight biclique in
54 polynomial time is impossible (Tan (2008)). Due to computational complexity
55 issues, methods based on random sampling have become popular (Mishra et al.
56 (2003), Suzuki and Tokuyama (2005)), but there are severe restrictions on the
57 size of the clusters in order to find them with high probability.

58 Despite the drawbacks, using bipartite graph based methods is important,

59 since besides clustering the objects, these have the potential of finding a subset
60 of relevant properties as well, and with this gives a detailed description of the
61 connection between the objects.

62 Our goal is to design an algorithm, that has the ability of detailed cluster
63 descriptions as bipartite graph based methods, but with polynomial running
64 time, without restrictions on the size of the clusters or the vertex degrees, and
65 application of randomized methods. The capability of handling overlaps be-
66 tween clusters and outliers is also required. So the desired output is not only
67 subsets of similar objects, but also subsets of properties, these objects (or a
68 large fraction of them) agree on.

69 We accomplish this by a three-phase algorithm, where both standard and
70 bipartite graphs are applied. The input is an object-property matrix, where
71 each row represents an object, showing which properties it has. This matrix
72 is converted into a standard weighted model (object distance graph), and a
73 bipartite model (object-property graph). Phase 1 is a modified MSF-based
74 clustering method on the standard weighted graph to find the seeds of the
75 clusters. These seeds are only subsets of the real clusters. Phase 2 consists of
76 two seed-refining step - one is carried out in the standard model, the other one
77 in the bipartite model. The role of Phase 3 is the clustering of objects based on
78 their similarities to the seeds.

79 The paper is organized as follows. In Section 2 some basic notations and
80 definitions are presented. In Section 3 the steps of the proposed method are
81 introduced. From Section 4 to 7 these steps are analyzed in details. Test results

of the algorithm are shown in Section 8. Section 9 presents the proof of a theoretical result for density bounds of subgraphs of bipartite graphs with size conditions.

2. Terminology and notation

Definition 1. An undirected graph $G = (V_G, E_G)$ consists of the set of vertices or nodes (V_G) , and E_G represents the edges.

Definition 2. A bipartite graph $G = (V, E) = (A, B, E)$ is a graph with two disjoint subset of vertices, such that $A \cup B = V$ and every edge connects a vertex in A to one in B .

Definition 3. Let G be a graph. If A is any subset of the vertex set, and v is any vertex, we denote by $N_A(v)$ the set of vertices adjacent to v in A .

Definition 4. Density of graphs. For a graph $G = (V, E)$ we define the density of G to be the quotient $\frac{|E|}{\binom{|V|}{2}}$. We also say that G has local density at least c (where c is any real number in the range $0 < c < 1$) if each vertex has degree at least $c(|V| - 1)$.

Definition 5. Density of bipartite graphs. For a bipartite graph $G = (V, E)$ with vertex bipartition $P \cup Q = V$, we define the density of G to be the quotient $\frac{|E|}{|P||Q|}$. We also say that G has local density at least c (where $0 < c < 1$) if each vertex $v \in P$ has at least $c|Q|$ neighbors in Q and each $v \in Q$ has at least $c|P|$ neighbors in P .

Definition 6. A connected component of a graph is a maximal subgraph such that any two vertices within are connected by a path (through a sequence of neighboring vertices).

Definition 7. An $F = (V_F, E_F)$ spanning tree of a $G = (V, E)$ is a spanning subgraph ($V_F = V$) and a tree (connected, cycle-free). A minimum weight spanning tree (MST) is a spanning tree with weight less than or equal to the weight

108 *of any other spanning tree. If the graph is not connected it contains a minimum*
109 *spanning forest (MSF).*

110 **3. Steps of the proposed algorithm**

111 In this section we will give a short overview of the steps of the proposed
112 algorithm (Figure 1).

113 Phase 1 is a cluster-seed mining process. The input is the data matrix,
114 which is used to build a distance graph. Each object is represented by a row
115 in the matrix, and each column corresponds to a property. The vertex set of
116 the distance graph consists of the objects, the edgeweights show the similarities
117 of the property vectors of the objects. The seeds are found by a MSF-based
118 method.

119 Phase 2 is the refining of the seeds. The seeds are splitted if necessary, by a
120 second MSF-based method. Then seeds are modeled in the bipartite graph with
121 the corresponding properties. Properties that are not representative enough will
122 be cut off. The output of this phase are the refined, bipartite seeds.

123 Phase 3 consists of computing the characteristic vectors of the seeds, and
124 clustering the objects based on these characteristics. The output of the al-
125 gorithm will be an object-cluster matrix, (in which each element shows how
126 strongly a given object belongs to a given cluster) and the cluster labels of the
127 vertices.

128 Our previous work (Keszler and Szirányi (2012)) was also based on using
129 both standard and bipartite graphs on the same dataset. However, there are

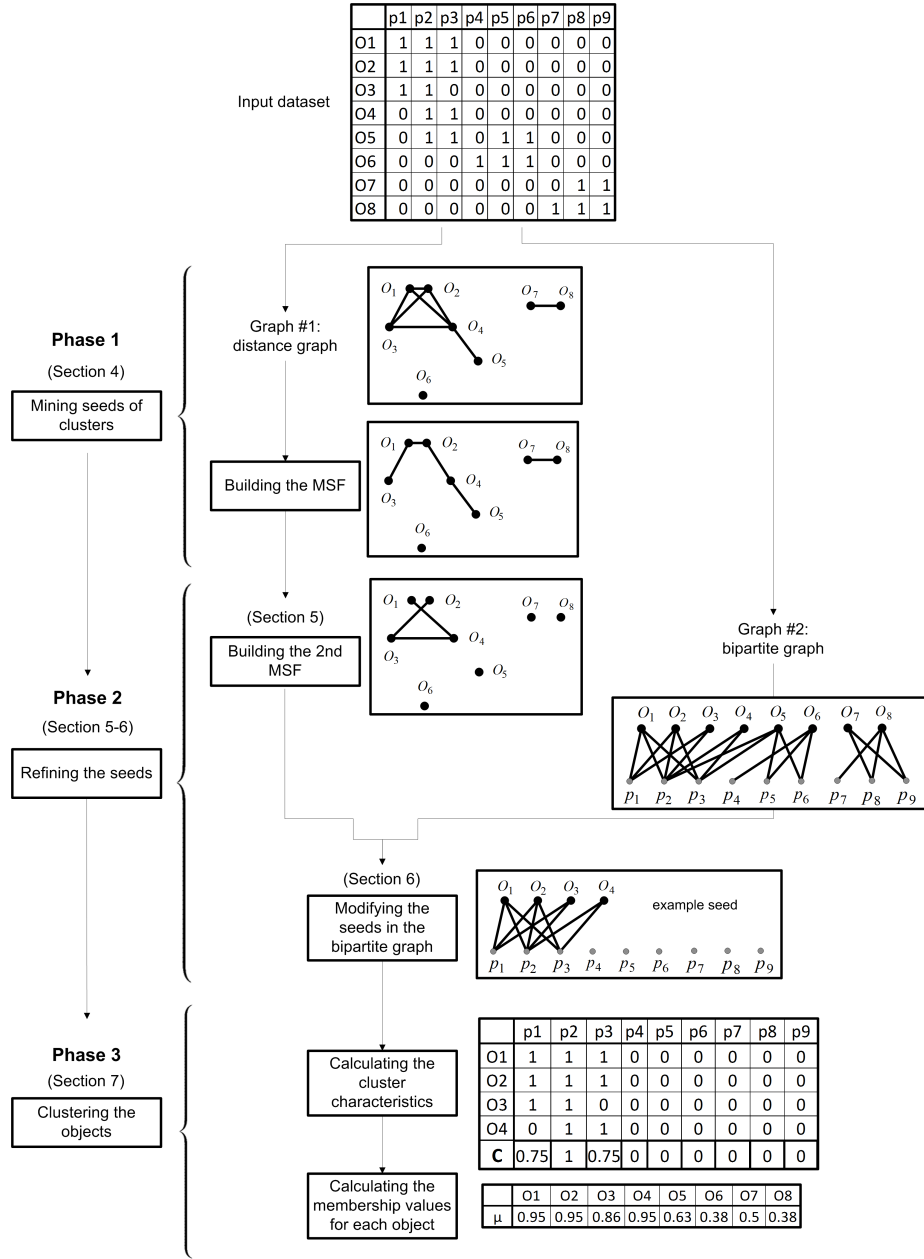


Figure 1: Flowchart of the proposed algorithm.

several important improvements presented in this paper. There was only one round of MSF applied. The second round is an important change, since with this and the stopping condition we can avoid clustering problems illustrated on Figure 2, such as detecting paths as cluster seeds. The selection of the stopping condition is also an improvement. The algorithm applied for refining the seeds is proved to be convergent with a polynomial running time on the number of vertices (Section 6.2.2). One of the most important improvements compared to the former paper are the theoretical results on the density bounds (Section 9).

The advantage of this algorithm structure is that each phase or substep can be replaced by a different one without effecting the others.

4. Mining seeds of clusters

The first step of the seed mining phase is to build the distance graph of objects. The distance values are calculated from the similarities of the property vectors. In case of binary properties, the edgeweight is equal to the number of properties the two vectors do not agree on.

The seed mining method is a modified MST-based (see Definition 7) clustering, using Kruskal's algorithm.

The basic idea behind clustering with MST is that the vertices connected by edges of small weight in the tree are likely to be in one cluster. Previous methods usually work by finding the MST, then cutting edges until a certain criteria is satisfied. This criteria can be a weight threshold (e.g. Chowdhury and Murthy (1997), Vathy-Fogarassy et al. (2006), Yujian (2007), Wang et al.

152 (2009), Zhou et al. (2011)), the number of clusters(e.g. Xu et al. (2001), Jia et al.
153 (2008), Peter (2012), Müller et al. (2012), one of the methods in Grygorash et al.
154 (2006)), the size of clusters (Laszlo and Mukherjee (2005)), or some intra-cluster
155 properties (e.g. Karthikeyan and Peter (2011), Goura et al. (2011)).

156 The above introduced papers were similar in the idea of first building the
157 MST and then cutting edges by a clustering criteria. However, there exist a few
158 bottom-up techniques as well.

159 An example of the bottom-up method is described in Felzenszwalb and Hut-
160 tenlocher (2004) and is applied for image segmentation. The output of this
161 algorithm is a partition of the vertex set.

162 Phase 1 of our algorithm also belongs to the bottom-up techniques. The main
163 difference between our method and the one in Felzenszwalb and Huttenlocher
164 (2004) is that our method is designed to handle outliers as well.

165 Our suggestion is to stop adding the edges when we reach the desired weight
166 threshold, instead of building the complete MST and then cutting off edges.
167 First we select a subgraph of the original graph by keeping the edges under the
168 weight threshold, then run the MST finding algorithm on each component of the
169 resulting graph. The advantage of this solution is that in the weight thresholded
170 graph each component can be processed in parallel.

171 The construction of the weighted graph from the input matrix is done in
172 $O(n^2 \cdot d)$, where n, d are the number of objects and properties respectively. The
173 running time of Phase 1 is $O(|E| \cdot \log|E|)$, since the edges are need to be sorted.
174 This is common in case of MSF-based methods.

175 The pseudo-codes to produce an MSF of a graph (Algorithm 1), and to find
 176 seeds in the weight-thresholded graph are presented below (Algorithm 2). If no
 177 threshold value is given, $w_{th} = avg_{e \in E}(w(e)) + std_{e \in E}(w(e))$ will be used, where
 178 avg is the average value, std is the standard deviation of the edgeweights.

Algorithm 1 MSF($G = (V, E)$) — Minimum weight spanning forest

Require: Distance graph $G = (V, E)$

Ensure: $F = (V_F, E_F)$, a MSF of G .

```

1:  $F = \emptyset$  {initialization}
2:  $E = SortEdgeWeights(E)$  {sorts edgeweights in increasing order}
3: for  $i = 1; i++ ; i \leq |E|$  do
4:   if  $e_i \in E : F \cup e_i$  is cycle-free then
5:      $F = F \cup e_i$ 
6: print  $F$ 

```

179 The next two sections will present in details the second phase, where the
 180 seeds will be modified. First, a second MSF building step is carried out (Section
 181 5), then the new set of seeds are processed in the bipartite graph (Section 6).

182 5. Refining the seeds - Building the 2nd MSF

183 Here, we apply a second MSF-building step, see Algorithm 3. The second
 184 MSF round is carried out by running Algorithm 2 on each seed found by the first
 185 round (Figure 1, Phase 2, step 1). The input of Algorithm 3 is a seed, and the
 186 corresponding MST. The edges of this MST will be removed, and the algorithm
 187 will be run on the remaining edge set. The new stopping condition will be

Algorithm 2 FINDSEED(G, w_{th}) — For finding cluster seeds in the distance graph

Require: Distance graph $G = (V, E)$, w_{th} edge weight threshold (optional)

Ensure: $G' = (V', E')$, such that $V' = V$, and $\forall e \in E' : w(e) \leq w_{th}$; and

$F = (V_F, E_F)$, a MSF of G' .

- 1: if w_{th} is not given, $w_{th} = \text{avg}_{e \in E}(w(e)) + \text{std}_{e \in E}(w(e))$; $V' = V$; $E' = \emptyset$.
 {initialization}
 - 2: **while** $\exists e \in E : w(e) \leq w_{th}$ **do**
 - 3: $E' = E' \cup e$
 - 4: $F = \text{MSF}(G' = (V', E'))$ {calling Algorithm 1}
 - 5: **print** G', F
-

188 calculated from the edge set of the first MST. The output of the algorithm run
189 on a seed will be a set of new seeds, since the original one might be splitted.

190 The threshold modification and the edge deletions are done in $O(|E|)$ for a
191 seed, and it can be carried out in parallel for each seed, so the running time of
192 this step is $O(|E|)$.

193 In Zhong et al. (2010) the authors also present a method of applying MST
194 building twice. The input of the second MSF algorithm is the original graph
195 without the edge set of the first MST. A second graph is built from the two
196 MST edge set, and vertices are separated by graph-cut.

197 Test results of the seed mining process, and the seed modification process in
198 the weighted standard graph are presented on Figure 2. The input dataset is a
199 weighted graph, the output are the seeds after the second round of MSF mining.

Algorithm 3 $\text{MODIFYSEED}(G', F)$ — For refining seeds in the distance graph

Require: $\{C_1, C_2, \dots, C_{N_C}\} :=$ components of G' (the output of Algorithm 2)

Ensure: $S = \{S_1, S_2, \dots\}$ set of cluster seeds

```

1: for  $i = 1; i++; i \leq N_C$  do

2:    $F_{2i} = \emptyset$  {initialization of the MSF for each component in  $G'$ }

3:    $w_{th2} = \text{avg}_{e \in E_F}(w(e)) + \text{std}_{e \in E_F}(w(e))$ 

4:   for  $i = 1; i++; i \leq N_C$  do

5:      $F_{2i} = \text{FINDSEED}((V_{C_i}, E_{C_i} \setminus E_F), w_{th2})$  {calling Algorithm 2}

6: print  $S$ 

```

200 The artificial input test datasets are illustrated on Figure 2(a). These test
 201 sets were constructed based on the typical distance based clustering problems
 202 mentioned in Zhong et al. (2010) and in Zahn (1971).

203 On Figure 2(b-e) the results of the first (left figures with red edges) and
 204 second (right figures with black edges) MSF rounds are shown for each input
 205 graph. After the second round, only the dense regions remain connected. The
 206 method can handle outliers (in contrast to graph partitioning methods), and
 207 applicable in case of cluster seeds of different sizes.

208 The drawback of several MST-based methods is that paths with small dis-
 209 tances between the neighboring vertices are detected as clusters. With our
 210 approach, these types of subgraphs will not be detected as dense regions, see
 211 Figure 2(e). This is the result of the modified threshold value in case of the
 212 second MSF round.

213 The second frequently appearing drawback of this type of algorithms, is
214 that overlapping clusters cannot be handled. This problem will be dealt with
215 in Phase 3 (see Section 7). At this phase, the cluster seeds are disjoint subsets
216 of the vertex (object) set.

217 Note that an object connected strongly to its neighboring objects might be
218 removed after the second MSF iteration. However, if this object belongs to that
219 dense region, it will be re-clustered in Phase 3. Examples will be presented in
220 Section 8.

221 **6. Refining the seeds - Modifying the seeds in the bipartite graph**

222 The seed mining phase, and the first step of the seed refining process is
223 finished. The next step is to model each seed as a bipartite graph, for further
224 analysis. One vertex class will be formed by the objects of the seed, and the
225 other one by the corresponding properties. The analysis consists of finding
226 objects and properties that do not belong strongly enough to the seed. This is
227 done by dense bipartite subgraph mining within each seed (Figure 1, Phase 2,
228 step 2).

229 *6.1. Previous methods*

230 Since finding bipartite cliques (bicliques) or counting them is an NP-complete
231 problem (Kutikov (2012)), some relaxations are needed to be made in order to
232 achieve lower computational complexity. Otherwise only exponential running
233 time algorithms exist, for example Zhang et al. (2008).

234 In Du et al. (2008) the authors present a method with a two-level clustering:
 235 first a seed mining step is carried out, then the remaining vertices are clustered.
 236 A bipartite graph is used for both steps, and the seeds are defined as the max-
 237 imal bicliques. The running time of their method is $O(|E|^2)$ on sparse graphs,
 238 however it is exponential in general. Other solutions, such as Tanay et al. (2002)
 239 or Dourisboure et al. (2009) reach polynomial running time by assuming lim-
 240 ited (constant) vertex degrees. In Geva and Sharan (2011) the biclique mining
 241 process is completed with a greedy expansion step. But within the seed identi-
 242 fication step, only small subsets of vertices are taken into consideration. If it is
 243 not necessary to gain overlapping clusters, further simplifications can be made
 244 (Suzuki and Wakita (2009)).

245 The size of the cluster might also be interesting, as in case of biclustering
 246 gene expression data (Mitra and Banka (2006)). If the expected size of the
 247 cluster is large enough compared to the whole dataset, random sample based
 248 methods are also applicable, e.g. Mishra et al. (2003).

249 *6.2. Our dense bipartite subgraph mining method*

250 We present known density bounds of subgraphs in bipartite graphs, then we
 251 introduce our dense bipartite subgraph mining method with a corresponding
 252 new theoretical result. The Dense Bipartite Subgraph lemma presents a lower
 253 bound on the reachable density value of a subgraph in a bipartite graph, with
 254 size conditions, however in applications this limit can be significantly higher.

255 Our approach for finding seeds is also a two-level method, such as Du et al.
 256 (2008), however for the first phase a standard graph is used, and the cluster seeds

257 in their method form complete bipartite subgraphs (bicliques). Our method is
 258 applicable regardless of the size or number of clusters. The running time of our
 259 method is quadratic in the number of vertices, see Section 9.

260 The final seeds will still be disjoint considering the object side of the bipartite
 261 graph, however overlaps between the property sets of the seeds might occur. On
 262 Figure 3 (b) the first seed shares properties with the second and the third one.

263 6.2.1. Density bounds of subgraphs in bipartite graphs

264 It is well known in graph theory that every graph of average degree d contains
 265 a subgraph of minimum degree at least $d/2$, and this bound is tight. Bipartite
 266 graphs with analogous properties can also be constructed.

267 Below we investigate the situation where, instead of prescribed minimum
 268 degree, we need to find a subgraph in which every vertex is required to be
 269 adjacent to at least a prescribed proportion of the other vertex class of the
 270 subgraph (Definition 5), and at least a positive given fraction is selected from
 271 each vertex class of the initial graph. Without the condition on the cardinalities
 272 of vertex classes, the problem would be rather simple because selecting any
 273 vertex together with its neighbors we obtain a subgraph (star) in which all
 274 vertices are completely joined with the other vertex class.

275 **Dense Bipartite Subgraph Lemma.** *Let c , r , and c' be reals such that*
 276 *$0 < r < c < 1$ and $c' \leq \frac{c-r}{1-r}$. Then every bipartite graph $G = (V, E)$ with*
 277 *density at least c contains a bipartite subgraph $G' = (V', E')$ with local density*
 278 *at least c' , such that $|P \cap V'| \geq r|P|$ and $|Q \cap V'| \geq r|Q|$, where P and Q denote*

279 the vertex classes of G . Moreover, a subgraph G' satisfying these conditions can
 280 be found in polynomial (more precisely, quadratic) time. (The proof is presented
 281 in Section 9.)

282 6.2.2. Modifying the seeds in the bipartite graph

283 To obtain the final seeds, density restrictions are made for each vertex indi-
 284 vidually in both vertex classes of the seeds (local density condition, see Definition
 285 5).

286 We apply Algorithm 4 on each seed, based on the principle that vertices (both
 287 objects and properties) not satisfying the degree constraint are successively
 288 removed. Note that removal changes the order of the corresponding vertex
 289 class, hence the situation may become better or worse for a vertex in the other
 290 class, depending on whether it was non-adjacent or adjacent to the vertex just
 291 removed. A check is performed, and deletions are only made if the density has
 292 grown.

293 The dense bipartite subgraph mining will be run on each seed, in parallel.
 294 After this step of the seed refining phase, each object will have a given proportion
 295 of the properties within each seed, and the same holds for the subset of properties
 296 belonging to that seed.

297 Once the algorithm stops, the degree constraints are automatically satisfied
 298 (otherwise the latest round of the **while** loops decreased n' and a further round
 299 will be performed). Hence, we need to show in the proof that this happens
 300 before any of the situations $|P'| < r|P|$ and $|Q'| < r|Q|$ occurs.

Algorithm 4 DENSEBIP(c, r, c') — Large locally dense bipartite subgraph

(assuming $0 < r < c < 1$ and $0 < c' \leq \frac{c-r}{1-r}$)

Require: Bipartite graph $G = (V, E)$ with vertex classes P, Q and density at least c

Ensure: Bipartite subgraph $G' = (V', E')$ with vertex classes $P' \subseteq P, Q' \subseteq Q$,

$|P'| \geq r|P|, |Q'| \geq r|Q|$, and local density at least c'

- 1: $P' := P, Q' := Q$ {initialization}
 - 2: $n' := |P'| + |Q'|$
 - 3: **while** $\exists x \in P' : |N_{Q'}(x)| < c'|Q'|$ **do**
 - 4: $P' := P' \setminus \{x\}$
 - 5: **while** $\exists x \in Q' : |N_{P'}(x)| < c'|P'|$ **do**
 - 6: $Q' := Q' \setminus \{x\}$
 - 7: **if** $|P'| + |Q'| < n'$ **then**
 - 8: **return to** 2
 - 9: **print** P', Q'
-

301 The running time of this step of Phase 2 is quadratic in the number of
 302 vertices of the bipartite graph modeling each seed (see Section 9). In case of an
 303 input matrix with size $n \times d$, the running time of this step is $O((n + d)^2)$. The
 304 process can be run in parallel on each seed as well.

305 The overall running time of Phase 2 (including Section 5) is $O(|E|) + O((n +$
 306 $d)^2) = O((n + d)^2)$, since $|E| = O(n^2)$.

307 This section completes the steps of the seed finding and refining phases of
 308 the algorithm. The last phase will be the clustering, where objects outside the
 309 seeds can also be clustered.

310 7. Clustering the objects

311 The output of Algorithm 4 is the final set of bipartite seeds. In this section
 312 we will present the idea of calculating the characteristics of clusters based on
 313 the seeds, and the method of calculating membership values for each object. As
 314 the final output, the algorithm provides an object-cluster matrix, in which each
 315 element represents the strength of connection between each object-cluster pair.

316 For each cluster, the characteristics is derived from the corresponding seed.
 317 In case of an $S = \{O_S, P_S, E_S\}$ seed, where O_S, P_S and E_S represents the set
 318 of objects, set of properties and set of edges respectively, the characteristics is
 319 calculated in the following way:

$$C_S(i) = \begin{cases} \sum_{o_j \in O_S} M_{ij} / |O_S|, & \text{if } p_i \in P_S \\ NULL, & \text{otherwise,} \end{cases} \quad (1)$$

320 where M is the input object-property matrix.

321 The membership values for the objects are derived from the similarities be-
 322 tween the cluster characteristic vectors and their property vectors. The simi-
 323 larities are evaluated only for the properties belonging to the seeds. The mem-
 324 bership value of object i with respect to the cluster with seed S_j is calculated
 325 as follows:

$$\mu_{ij} = \sum_{p_k \in P_{S_j}} |M_{ik} - C_{S_j}(k)| \quad (2)$$

326 If an object reaches a membership value as high as the minimum membership
 327 values of the objects of the corresponding seed, it will be clustered. The rest
 328 of the objects will not be clustered automatically. The minimum of the mem-
 329 bership values necessary for clustering depends on the application. Since an
 330 object might reach the threshold of clustering in case of more than one cluster,
 331 overlaps might occur.

332 Since each object belongs to at most one seed, the time complexity of calcu-
 333 lating the characteristics is $O(n \cdot d)$. (As Phase 2, this can be run in parallel on
 334 each seed.) Clustering the objects is done in $O(n^2 \cdot d)$, which is the algorithmic
 335 complexity of this phase.

336 With parallelization the overall running time of the three-phased method is:
 337 $O(|E| \cdot \log|E|) + O(n + d)^2 + O(n^2 \cdot d) = O(n^3) + O(n + d)^2 + O(n^2 \cdot d)$.

338 8. Test results

339 In this section test results on synthetic and real-world datasets are also
340 presented.

341 8.1. Synthetic example

342 An artificial test dataset is introduced on Figure 3a. The dataset was con-
343 structed in order to demonstrate the effectiveness of our method in finding
344 similar objects, and in selecting relevant subset of properties (dense bipartite
345 subgraphs).

346 The bipartite graph (26 objects, 24 properties) contains 2 bicliques ($O_{11}-O_{15}$
347 and $O_{16}-O_{20}$), and one with additional properties (O_1-O_{10}). The fourth
348 subgraph is a counter example ($O_{21}-O_{26}$). These subgraphs are marked with
349 black, the remaining edges (gray) were selected randomly.

350 On Figure 3 the results of the seed mining and refining steps are presented.
351 The three dense regions were detected by our method, with the automatic
352 threshold used in Algorithm 2 and 3. On Figure 3b the output of the second
353 MSF round is shown: the seeds are highlighted in bold. Note that some ob-
354 jects of the dense regions were not selected (second seed), and the seeds contain
355 additional properties.

356 The latter problem is solved in Phase 2 by applying Algorithm 4. The
357 parameter r was set to 0.75, that is, at least 75% of the properties and objects
358 in each seed are needed to be kept. (This setting depends on how dense and
359 large subgraphs do we want to gain as clusters.) The output of this seed refining

step is presented on Figure 3c. The additional loosely connected properties were ruled out in case of the second and third seeds, however some remained in case of the first.

However, we still have lost objects, that should have been selected by the seed-finding step. This problem was mentioned at the end of Section 5, and is solved by Phase 3 of the algorithm. In case of each seed the characteristics and the membership values of each object-cluster pair were calculated. The results are presented on Figure 3d. Besides the original seed vertices, other objects are also clustered.

8.2. Application related datasets

8.2.1. Test results on DIMACS datasets

The method was also tested on real-world datasets (free-access DIMACS datasets (Dolphins (Lusseau et al. (2003)), Jazz (Gleiser and Danon (2003)), Football (Girvan and Newman (2002))), see Tables 1 and 2.

The Dolphins dataset describes the interaction between 62 dolphins. The object-property matrix is constructed as follows: the i^{th} row shows the dolphins which the i^{th} dolphin is interacting with (1 - interaction, 0 - no interaction). Our goal is to find subgroups of dolphins with dense connection systems. The Jazz dataset contains the co-operating network of 198 jazz musicians (2742 edges). The Football dataset describes the network of football games between 115 teams. The goal in both cases is finding dense regions within the dataset. In the head of each subtable the average density of the corresponding dataset is also noted.

Table 1 presents the results on the Dolphins dataset. The gained cluster seeds after the 2nd MSF round (Phase 2, step 1 of our method) are significantly denser compared to the average density of the dataset (Table 1a). The density of the final seeds (output of Phase 2) have been further increased. The results corresponding to the stopping condition for Algorithm 2 are highlighted in bold. The final clusters (Phase 3) are presented in Table 1b with the identifier of the dolphins. The dolphins appearing in both clusters are highlighted in bold.

Note that the seed refining steps of Phase 2 resulted in an increased density. Furthermore, the cluster density values of the suggested stopping condition are higher or at least as high as other settings below and above this threshold. The capability of handling outliers and overlaps between clusters are also illustrated in Table 1b.

Test results of the other two datasets are presented in Table 2.

8.2.2. Comparison with other methods

Our algorithm was compared to other clustering methods by using the commonly tested Southern Women dataset (Freeman (2003)), in what the social activities (14 events) of 18 women was documented, see Figure 5. The advantage of our method compared to Barber et al. (2008) and Suzuki and Wakita (2009) is the capability of handling overlaps between clusters, see Figure 5d. Du et al. (2008) also detects overlapping clusters, but the resulting densities are significantly lower than our results. However, their method clusters all objects, while ours detect outliers that did not correspond strongly enough to the clusters. The advantage of our seed mining method is that the seeds do not need

Table 1: Test results on real-world datasets.

Results with the stopping condition for the MSF building phase, see Algorithm 2) are highlighted in bold. Results of lower and higher threshold values are shown before and after this, respectively. The size parameter r was set to 0.75 (see Dense Bipartite Subgraph Lemma). The density of the final seeds are significantly higher than the average density of the dataset. Columns: number of seeds (N), number of objects within each seed (size), density after first refining step, final seed size and density.

(b) Dolphins dataset - Results of

Phase 3 (final clusters). Dol-

(a) Dolphins dataset - Results of the two seed
refining steps (see Phase 2).

phins appearing in both clusters
are highlighted in bold.

Dolphins dataset - Average density 0.0827				
Seeds - 2 nd MSF round			Final seeds	
N	objects	density	objects	density
5	3	0.11	3	0.15
	4	0.15	4	0.20
	2	0.129	2	0.17
	2	0.129	2	0.17
	6	0.131	6	0.173
2	9	0.11	9	0.15
	18	0.129	18	0.17
1	47	0.10	47	0.125

Seed	Dolphins in two clusters
1st	19 ,22,24,25,30, 46 , 51 ,52
2nd	14-19, 34-41, 44-46, 51

Table 2: Further test results on real-world datasets. Notation is the same as in

Table 1

(a) Football dataset

Football dataset - Average density 0.0927				
Seeds - 2 nd MSF round			Final seeds	
N	objects	density	objects	density
11	8	0.096	8	0.126
	10	0.096	10	0.126
	11	0.093	11	0.123
	4	0.089	4	0.118
	8	0.094	8	0.124
	9	0.094	9	0.124
	11	0.1	11	0.13
	2	0.096	2	0.126
	9	0.1	9	0.13
	10	0.092	10	0.12
	2	0.091	2	0.12
9	18	0.096	18	0.126
	12	0.094	12	0.124
	13	0.09	13	0.12
	12	0.093	12	0.122
	8	0.093	8	0.124
	9	0.094	9	0.124
	11	0.98	11	0.13
	9	0.093	9	0.122
	9	0.99	9	0.13

(b) Jazz dataset

Jazz dataset - Average density 0.1399				
Seeds - 2 nd MSF round			Final seeds	
N	objects	density	objects	density
1	62	0.24	62	0.30
1	128	0.186	128	0.235
1	162	0.16	122	0.16
1	162	0.16	162	0.20

405 to be complete subgraphs, therefore it is applicable in the presence of noise as
406 well.

407 The method of Du et al. (2008) was compared to ours on the example de-
408 scribed in Section 8.1. Figure 4c presents the result of their method. The seeds
409 in their version are maximal bicliques, and the figure shows the 14 largest ones.
410 In this case the final clusters were the seeds themselves. The results clearly show,
411 that although their clusters are denser than ours, they split the vertices into too
412 many parts. In contrast with their method, ours is capable of contracting seeds
413 (in Phase 3).

414 Another comparison was carried out on the Dolphins dataset presented in
415 Section 8.2.1. The adjacency matrix of the bipartite graph and some examples
416 of the seeds found by (Du et al. (2008)) are presented on Figures 4d and 4e. Since
417 the graph is sparse, and the overlap between the neighborhood of the dolphins
418 is small, the biclique-enumeration based method finds a large number of small
419 seeds. Due to the number of these seeds, only some of the largest are shown.
420 Our method found two clusters, and the results were detailed in Table 1.

421 As a conclusion, the advantage of our method compared to modularity-based
422 techniques is that it is able to find overlapping clusters or outliers as well. On
423 the other hand, compared to the two-level biclique-mining method it is more
424 suitable to work in case of noise or in sparse graphs, since our method can
425 detect a dense subgraph (compared to the average density of the graph) even if
426 it does not contain maximal bicliques. Also note that in case of dense graphs,
427 enumerating all bicliques would be quite inefficient, in contrast to ours that has

polynomial running time regardless of the density.

9. Proof of the Dense Bipartite Subgraph Lemma

Here we present the proof of the Dense Bipartite Subgraph Lemma.

Suppose that the **while** loops are performed exactly k times during the algorithm. For $i = 1, 2, \dots, k$ let p_i and q_i denote the number of vertices removed from P' and Q' , respectively, in the i th round of the **while** loops. (Some of them, namely p_1 , p_k , and/or q_k may be zero.) Let us further denote $p := |P|$, $q := |Q|$, $p' := |P'|$, $q' := |Q'|$. By assumption, $|E| \geq cpq$. We observe that

- removing the p_i vertices from P' , fewer than $c'p_i(q - \sum_{1 \leq j < i} q_j)$ edges are deleted;
- removing the q_i vertices from Q' , fewer than $c'q_i(p - \sum_{1 \leq j \leq i} p_j)$ edges are deleted.

These are direct consequences of the conditions given in lines 3 and 5 of the algorithm. When the algorithm stops, $|E_{del}|$, the number of edges deleted altogether is less than

$$|E_{del}| < \sum_{i \geq 1} c'p_i(q - \sum_{1 \leq j < i} q_j) + \sum_{i \geq 1} c'q_i(p - \sum_{1 \leq j \leq i} p_j) \quad (3)$$

The right hand side can be rewritten as

$$\begin{aligned} & c'(p_1q + q_1(p - p_1) + p_2(q - q_1) + q_2(p - p_1 - p_2) + \dots \\ & + p_k(q - q_1 - \dots - q_{k-1}) + q_k(p - p_1 - \dots - p_k)) \end{aligned} \quad (4)$$

With further rearrangements, using that $p = \sum_{i \geq 1} p_i + p'$, and $q = \sum_{i \geq 1} q_i + q'$ we get:

$$\begin{aligned}
|E_{del}| &< c'((p - p')q + (q - q')p - \\
&\quad - (p_1 + \dots + p_k)(q_1 + \dots + q_k)) \\
|E_{del}| &< c'((p - p')q + (q - q')p - (p - p')(q - q')) \\
|E_{del}| &< c'(pq - p'q')
\end{aligned} \tag{5}$$

Thus, the number of edges remaining in G' is

$$|E'| > cpq - c'(pq - p'q') = (c - c')pq + c'p'q'. \tag{6}$$

This $|E'|$ cannot exceed $p'q'$, hence after rearrangement we obtain

$$\begin{aligned}
(c - c')pq &< (1 - c')p'q', \\
\frac{c - c'}{1 - c'} &< \frac{p'q'}{pq}.
\end{aligned} \tag{7}$$

On the other hand, if at least one of the inequalities $p' < rp$ and $q' < rq$ is valid, then we necessarily have $p'q' < rpq$ (because $p' \leq p$ and $q' \leq q$ always hold). Consequently, in that case we would have

$$\begin{aligned}
\frac{c - c'}{1 - c'} &< r, \\
c - c' &< r - rc', \\
c - r &< c'(1 - r), \\
c' &> \frac{c - r}{1 - r},
\end{aligned} \tag{8}$$

444 contradicting the assumption of the lemma. Thus, both $p' \geq rp$ and $q' \geq rq$
445 are valid.

446 The conditions for executing the steps purely depend on vertex degrees,
447 which can be evaluated in linear time; moreover, at most $(1 - r)|V|$ vertices
448 can be removed (i.e., $k \leq (1 - r)|V|$ holds for the number of rounds for the
449 **while** loops). Thus, the overall running time of the algorithm is polynomial
450 (quadratic).

451 10. Conclusions

452 We have introduced a dense subgraph mining method in bipartite graphs
453 using the advantages of both the standard and the bipartite graph models. The
454 algorithm consists of three main phases: a seed mining in a standard graph, a
455 seed refining phase both in the standard and bipartite model and a clustering
456 phase. Our method is applicable for clusters of any size, and the number of
457 clusters is not need to be fixed either. It is able to detect overlapping clusters
458 and outliers in bipartite graphs such as dense bipartite mining methods (in
459 contrast with graph partitioning techniques), but with polynomial running time.
460 Test were run on synthetic and real-world datasets as well, presented in Section
461 8. Besides the clustering method, new theoretical results on density bounds
462 of subgraphs in bipartite graphs with size and local density constraints are
463 discussed as well. In the future, further analysis and tests on the optimal size
464 of clusters will be carried out for more application areas.

465 **References**

- 466 Barber, M. J., Faria, M., Streit, L., and Strogan, O. (2008). Searching for
467 communities in bipartite networks. In Bernido, C. C. and Bernido, V. C.,
468 editors, *Searching for Communities in Bipartite Networks: Proceedings of*
469 *the 5th Jagna International Workshop*, volume 1021, pages 171–182. AIP
470 Conf. Proc.
- 471 Benchettara, N., Kanawati, R., and Rouveirol, C. (2010). Supervised machine
472 learning applied to link prediction in bipartite social networks. In *Proceedings*
473 *of 2010 International Conference on Advances in Social Networks Analysis*
474 *and Mining*, pages 326–330. IEEE.
- 475 Boykov, Y. and Kolmogorov, V. (2004). An experimental comparison of min-
476 cut/max-flow algorithms for energy minimization in vision. *IEEE Trans.*
477 *Pattern Anal. Mach. Intell.*, 26(9):1124–1137.
- 478 Chowdhury, N. and Murthy, C. (1997). Minimum spanning treebased clus-
479 tering technique: Relationship with bayes classifier. *Pattern Recognition*,
480 30(11):1919–1929.
- 481 Cousty, J., Bertrand, G., Najman, L., and Couprie, M. (2009). Watershed cuts:
482 Minimum spanning forests and the drop of water principle. *IEEE Transac-*
483 *tions on Pattern Analysis and Machine Intelligence*, 31:1362–1374.
- 484 Cousty, J., Bertrand, G., Najman, L., and Couprie, M. (2010). Watershed
485 cuts: Thinnings, shortest path forests, and topological watersheds. *IEEE*
486 *Transactions on Pattern Analysis and Machine Intelligence*, 32:925–939.

487 Danek, O., Matula, P., Maska, M., and Kozubek, M. (2012). Smooth chan-veye
488 segmentation via graph cuts. *Pattern Recognition Letters*, 33(10):1405–1410.

489 Dourisboure, Y., Geraci, F., and Pellegrini, M. (2009). Extraction and classi-
490 fication of dense implicit communities in the web graph. *ACM Trans. Web*,
491 3(2):7:1–7:36.

492 Du, N., Wang, B., Wu, B., and Wang, Y. (2008). Overlapping community
493 detection in bipartite networks. In *Web Intelligence*, pages 176–179. IEEE.

494 Feige, U. (2004). Approximating maximum clique by removing subgraphs. *SIAM*
495 *J. Discrete Math.*, 18(2):219–225.

496 Felzenszwalb, P. F. and Huttenlocher, D. P. (2004). Efficient graph-based image
497 segmentation. *Int. J. Comput. Vision*, 59(2):167–181.

498 Freeman, L. C. (2003). Finding social groups: A meta-analysis of the south-
499 ern women data. In *Dynamic Social Network Modeling and Analysis. The*
500 *National Academies*, pages 39–97.

501 Geva, G. and Sharan, R. (2011). Identification of protein complexes from co-
502 immunoprecipitation data. *Bioinformatics (Oxford, England)*, 27(1):111–117.

503 Girvan, M. and Newman, M. E. J. (2002). Community structure in social and
504 biological networks. *Proceedings of the National Academy of Sciences of the*
505 *United States of America*, 99(12):7821–7826.

506 Gleiser, P. and Danon, L. (2003). Advanced complex systems. (6):565.

507 Goura, V. M. K. P., Rao, N. M., and Reddy, M. R. R. (2011). A dynamic
508 clustering technique using minimum-spanning tree. *IPCBEE*, 7:66–70.

509 Grygorash, R., Zhou, Y., and Jorgensen, Z. (2006). Minimum spanning tree
510 based clustering algorithms. In *Proceedings of the 18th IEEE International
511 Conference on Tools with Artificial Intelligence (ICTAI06)*, pages 73–81.

512 Jain, A. K. (2010). Data clustering: 50 years beyond k-means. *Pattern Recog-
513 nition Letters*, 31(8):651–666.

514 Jancura, P. and Marchiori, E. (2010). Dividing protein interaction networks for
515 modular network comparative analysis. *Pattern Recogn. Lett.*, 31(14):2083–
516 2096.

517 Jia, Y., Wang, J., Zhang, C., and Hua, X.-S. (2008). Augmented tree partition-
518 ing for interactive image segmentation. In *ICIP*, pages 2292–2295. IEEE.

519 Karthikeyan, T. and Peter, S. J. (2011). Edge connectivity based clustering
520 through minimum spanning tree. 1(2):57–61.

521 Keszler, A. and Szirányi, T. (2012). A mixed graph model for community detec-
522 tion. *International Journal of Intelligent Information and Database Systems*,
523 page In Press.

524 Kutzkov, K. (2012). An exact exponential time algorithm for counting bipartite
525 cliques. *Inf. Process. Lett.*, 112(13):535–539.

526 Laszlo, M. and Mukherjee, S. (2005). Minimum spanning tree partitioning

algorithm for microaggregation. *IEEE Transactions on Knowledge and Data Engineering*, 17(7):902–911.

Lusseau, D., Schneider, K., Boisseau, O. J., Haase, P., Slooten, E., and Dawson, S. M. (2003). The bottlenose dolphin community of Doubtful Sound features a large proportion of long-lasting associations. *Behavioral Ecology and Sociobiology*, 54(4):396–405.

Mishra, N., Ron, D., and Swaminathan, R. (2003). On finding large conjunctive clusters. In *COLT*, pages 448–462.

Mitra, S. and Banka, H. (2006). Multi-objective evolutionary biclustering of gene expression data. *Pattern Recognition*, 39(12):2464 – 2477. Bioinformatics.

Müller, A. C., Nowozin, S., and Lampert, C. H. (2012). Information theoretic clustering using minimum spanning trees. In *DAGM/OAGM Symposium*, volume 7476 of *Lecture Notes in Computer Science*, pages 205–215. Springer.

Peter, S. J. (2012). Local density-based hierarchical clustering for overlapping distribution using minimum spanning tree. *International Journal of Computer Applications*, 43(12):7–11. Published by Foundation of Computer Science, New York, USA.

Schaeffer, S. E. (2007). Graph clustering. *Computer Science Review*, 1(1):27 – 64.

Suzuki, A. and Tokuyama, T. (2005). Dense subgraph problems with output-

- density conditions. In *ISAAC*, volume 3827 of *Lecture Notes in Computer Science*, pages 266–276. Springer.
- Suzuki, K. and Wakita, K. (2009). Extracting multi-facet community structure from bipartite networks. In *Proceedings of the 2009 International Conference on Computational Science and Engineering - Volume 04*, CSE '09, pages 312–319, Washington, DC, USA. IEEE Computer Society.
- Tan, J. (2008). Inapproximability of maximum weighted edge biclique and its applications. In *TAMC'08: Proceedings of the 5th international conference on Theory and applications of models of computation*, pages 282–293, Berlin, Heidelberg. Springer-Verlag.
- Tanay, A., Sharan, R., and Shamir, R. (2002). Discovering statistically significant biclusters in gene expression data. In *In Proceedings of ISMB 2002*, pages 136–144.
- Vathy-Fogarassy, A., Kiss, A., and Abonyi, J. (2006). Hybrid minimal spanning tree and mixture of gaussians based clustering algorithm. In *Foundations of Information and Knowledge Systems*, volume 3861 of *Lecture Notes in Computer Science*, pages 313–330. Springer Berlin / Heidelberg.
- Wang, X., Wang, X., and Wilkes, D. M. (2009). A divide-and-conquer approach for minimum spanning tree-based clustering. *IEEE Transactions on Knowledge and Data Engineering*, 21:945–958.
- Xu, Y., Olman, V., and Xu, D. (2001). Minimum spanning trees for gene expression data clustering. *Genome Informatics*, 12:24–33.

- 570 Yujian, L. (2007). A clustering algorithm based on maximal θ -distant subtrees.
571 *Pattern Recognition*, 40(5):1425 – 1431.
- 572 Zahn, C. (1971). Graph-theoretical methods for detecting and describing gestalt
573 clusters. *IEEE Transactions on Computers*, pages 68–86.
- 574 Zhang, Y., Chesler, E. J., and Langston, M. A. (2008). On finding bicliques
575 in bipartite graphs: a novel algorithm with application to the integration of
576 diverse biological data types. In *Proceedings of the 41st Hawaii International*
577 *Conference on System Sciences*, pages 473–481. IEEE Computer Society.
- 578 Zhong, C., Miao, D., and Wang, R. (2010). A graph-theoretical clustering
579 method based on two rounds of minimum spanning trees. *Pattern Recognition*,
580 43(3):752 – 766.
- 581 Zhou, Y., Grygorash, O., and Hain, T. F. (2011). Clustering with mini-
582 mum spanning trees. *International Journal on Artificial Intelligence Tools*,
583 20(1):139–177.

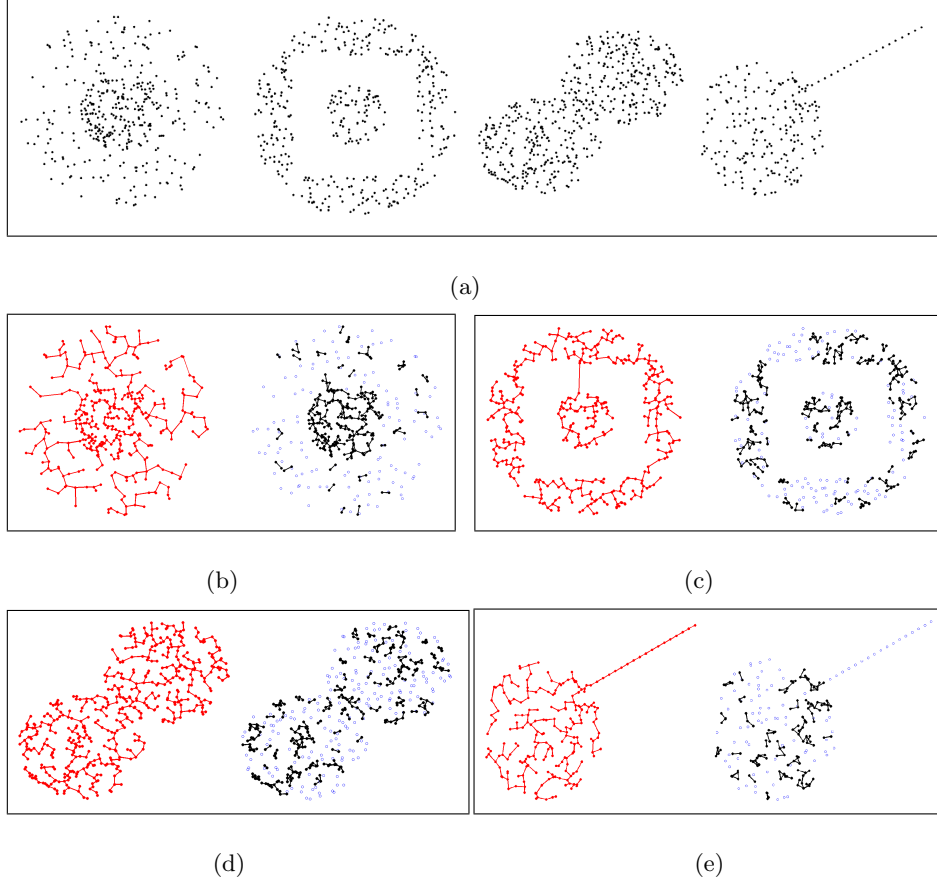
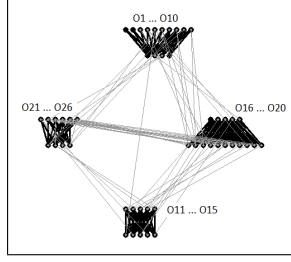
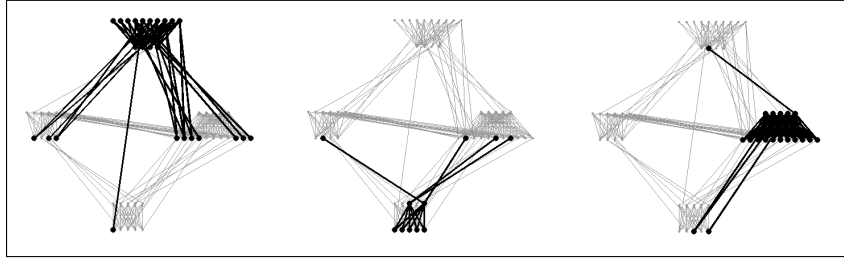


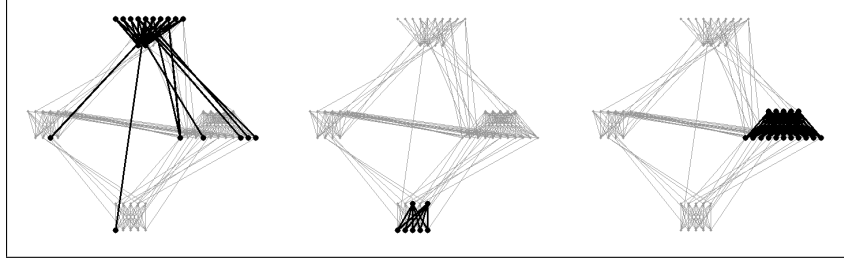
Figure 2: Test results of seed mining process. The four input graphs (a), and the result of the seed mining process (b-e). The output of the first MSF building phase are shown in red (left), the output of the second MSF building phase are shown in black (right). Only the densest regions remain connected.



(a) Test graph (26 objects, 24 properties).



(b) Seeds: output of the second MSF building step (Phase 2, step 1).

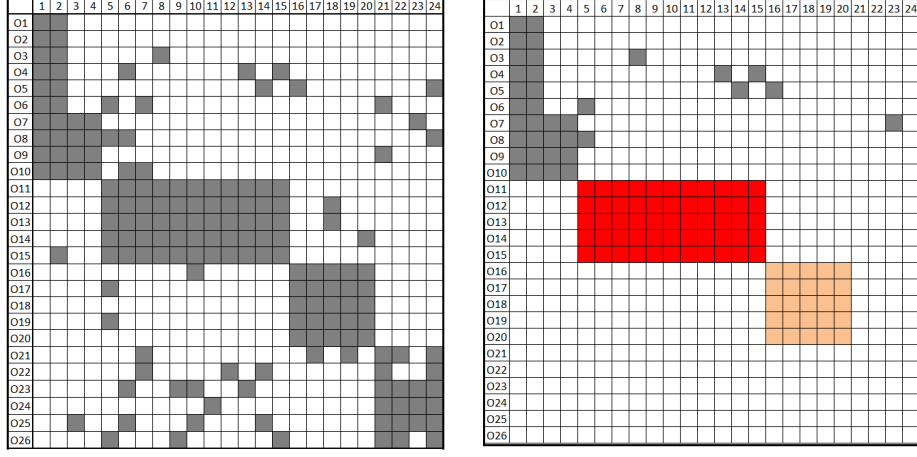


(c) Seeds after the seed refining process (Phase 2, step 2). Overlaps occur between the property set of the seeds.

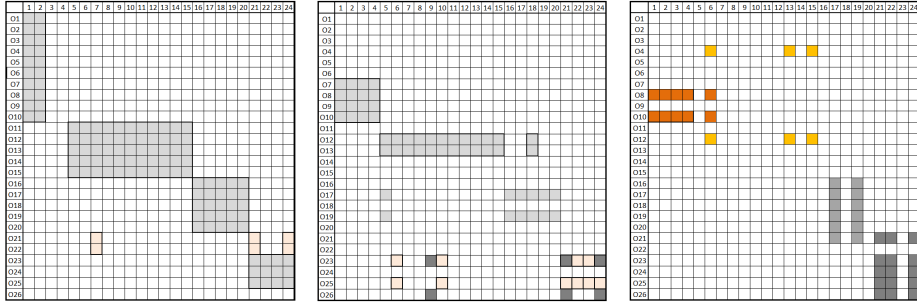
	O1	O2	O3	O4	O5	O6	O7	O8	O9	O10	O11	O12	O13	O14	O15	O16	O17	O18	O19	O20	O21	O22	O23	O24	O25	O26
C1	0,96	0,96	0,91	0,87	0,87	0,92	0,91	0,92	0,96	0,96	0,41	0,36	0,36	0,36	0,47	0,52	0,46	0,47	0,4	0,52	0,68	0,74	0,59	0,69	0,64	0,66
C2	0,43	0,43	0,48	0,57	0,38	0,48	0,29	0,38	0,29	0,43	1	1	1	1	1	0,38	0,38	0,43	0,33	0,76	0,29	0,48	0,48	0,33	0,38	0,48
C3	0,61	0,61	0,56	0,5	0,61	0,44	0,5	0,44	0,5	0,44	0,28	0,33	0,33	0,33	0,22	1	1	1	1	1	0,72	0,5	0,56	0,61	0,56	0,5
Cluster ID	C1	C1	C1	C1	C1	C1	C1	C1	C1	C1	C2	C2	C2	C2	C2	C3	C3	C3	C3	C3						

(d) Final clusters($C1 - C3$). Cluster-membership values for objects $O_1 - O_{26}$. Seeds are marked in each cluster. O_{11}, O_{12} and O_{14} were also clustered, besides the seed of $C2$.

Figure 3: The output of our method phase by phase on a test graph.

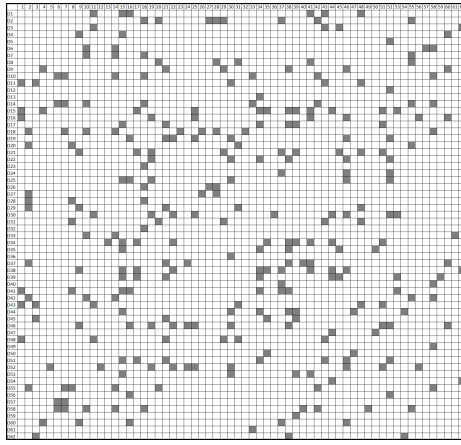


(a) The adjacency matrix of the test graph on Figure 3a (edges are marked by dark gray cells). (b) The output of our method, the three clusters are marked in the adjacency matrix.

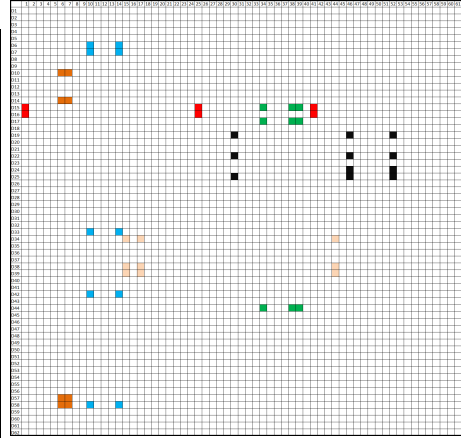


(c) Results of (Du et al. (2008)) on input Fig. 4a. The 14 largest clusters are marked on three subfigures. Example: the light orange cluster on the right side is a biclique of objects O_4, O_{12} and properties p_6, p_{13}, p_{15} . The data set is highly over segmented.

Figure 4

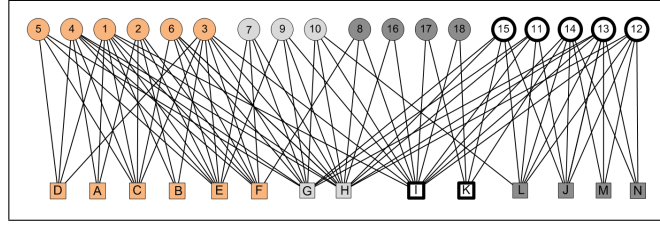


(d) Adjacency matrix of the Dolphins dataset. Dark cells denote the edges.

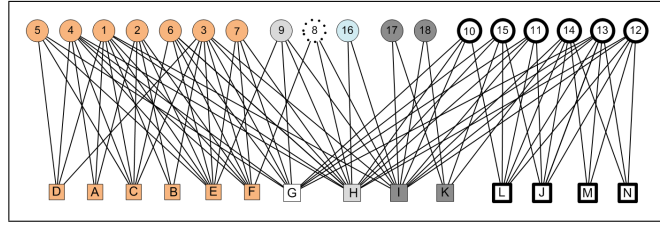


(e) Example cluster seeds of method Du et al. (2008) on the Dolphins dataset, marked by different colors.

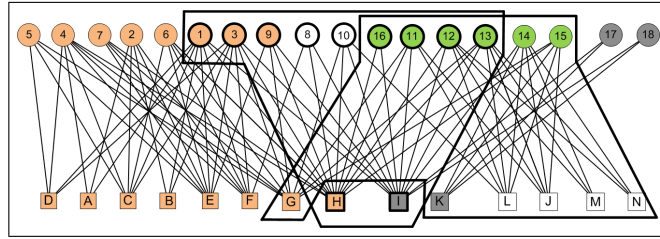
Figure 4: Test results on the artificial dataset presented on Figure 3a and on the DIMACS Dolphins dataset.



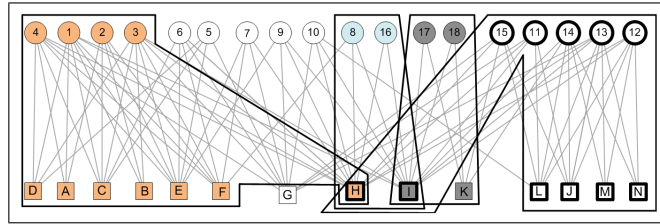
(a) Barber et al. (2008) - No overlaps or outliers.



(b) Suzuki and Wakita (2009) - No overlaps or outliers.



(c) Du et al. (2008) - Overlaps are handled. The density of clusters: 0.64, 0.66, 1 and 1.



(d) Result of our method. Overlaps are handled. The density of clusters: 0.8, 0.89, 1 and 1. Outliers were detected.

Figure 5: Test results on the Southern Women dataset. The object set contains 18 women, the property set models 14 social event they attended.